



SEQ ID NO: 31

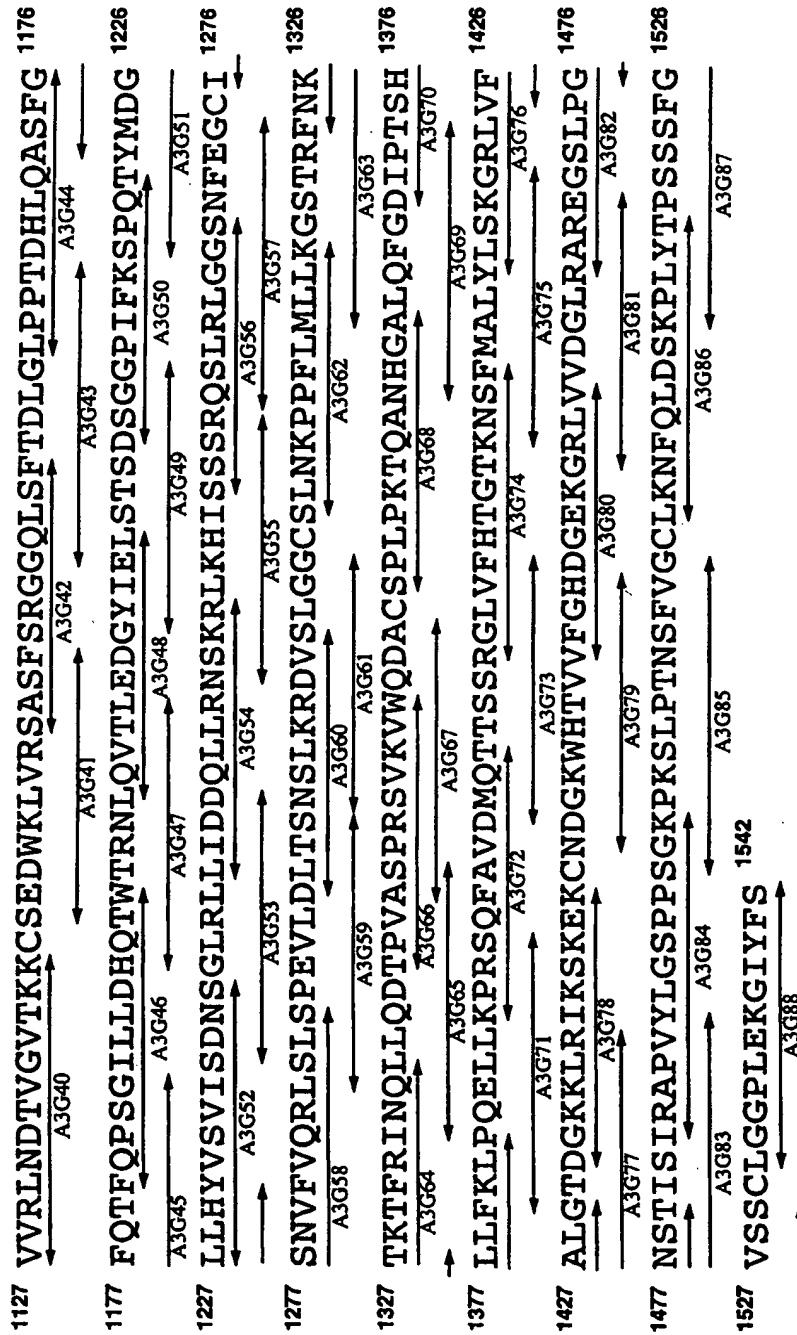


Figure 5

SER ID NO: 32

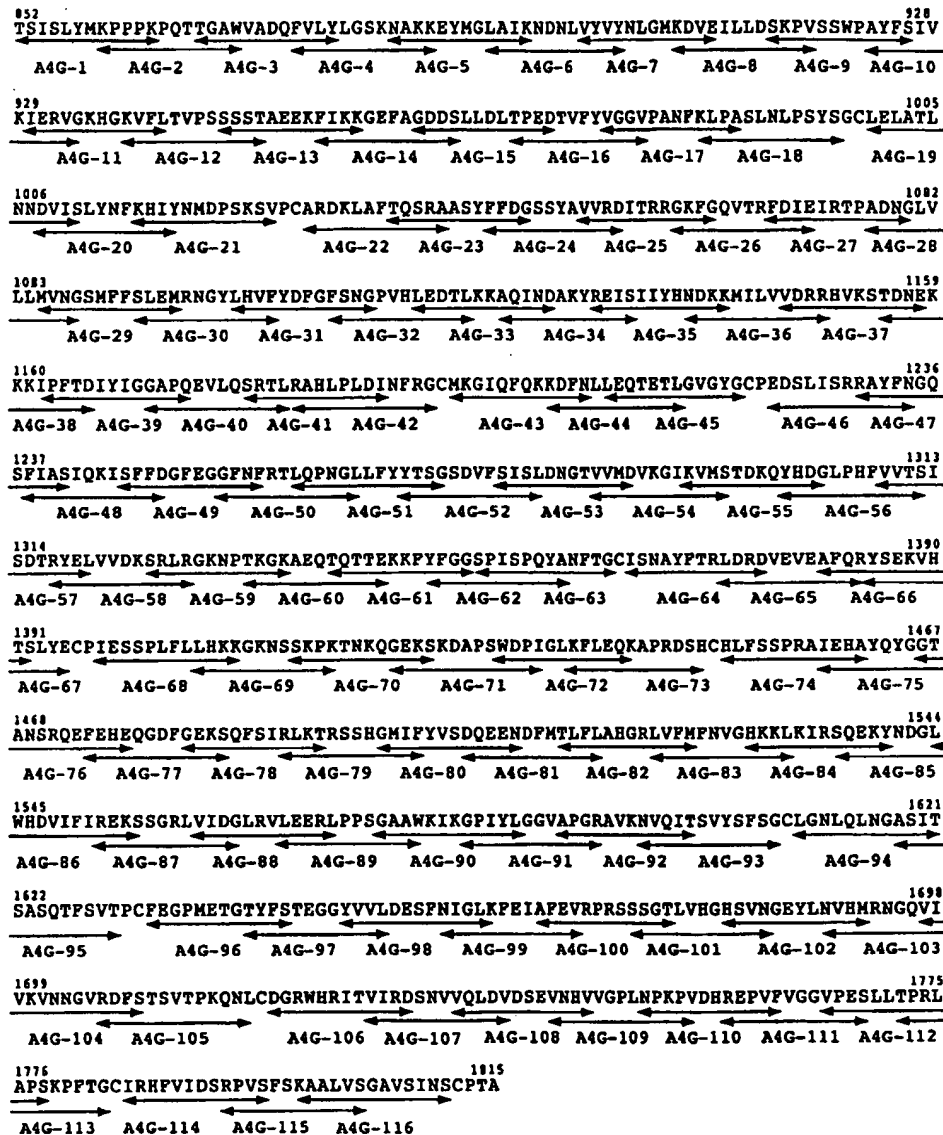


Figure 6

SEQ ID NO: 33

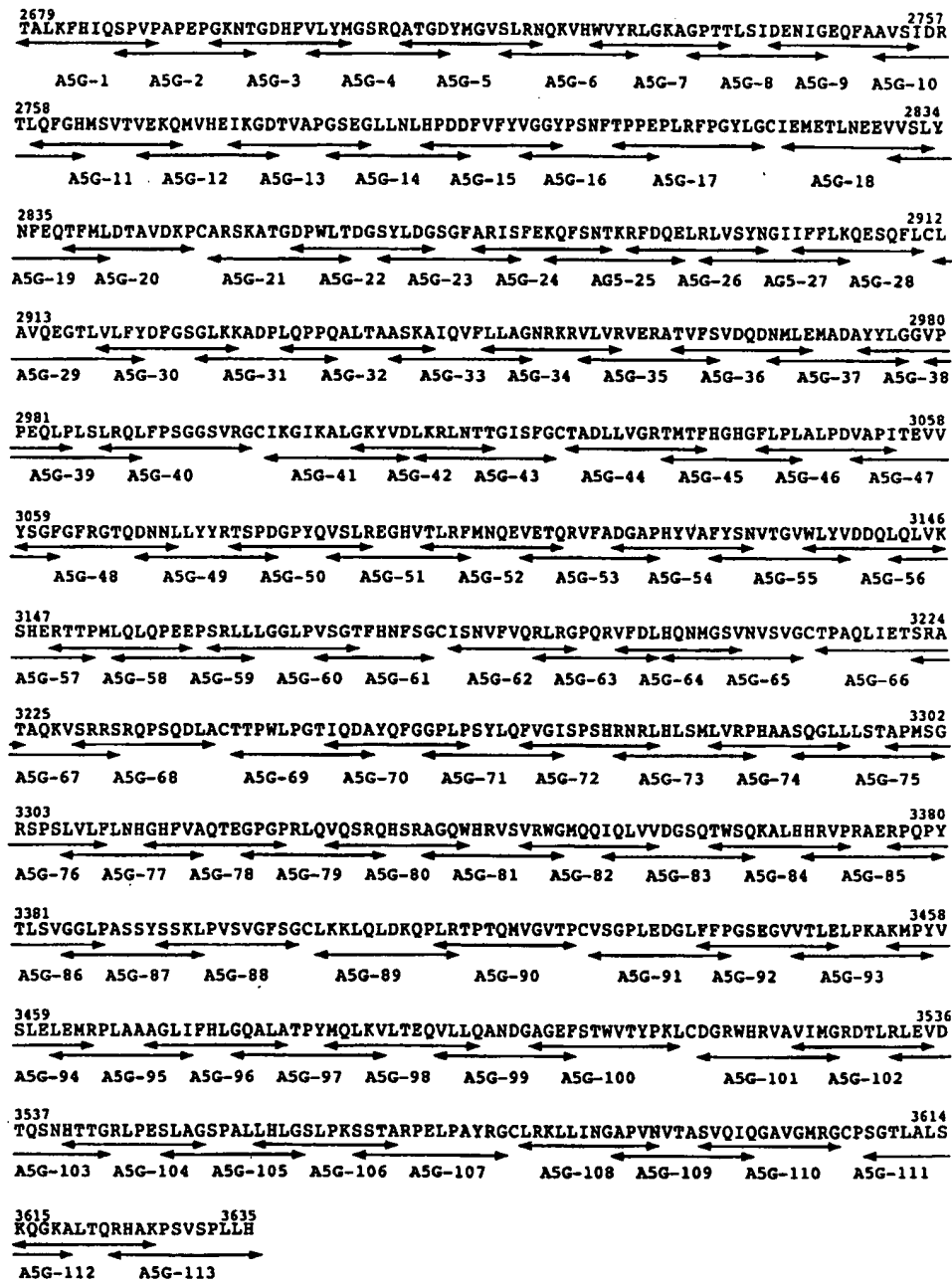


Figure 7

PEPTIDES	Laminin Chain and Amino Acid Sequence Number	Amino Acid Sequence	% Disruption/ Disassembly of Fibrillar AB (AB:Peptide Molar Ratio of 1:6)	SERID
AG73	Alpha-1 chain; residues 2719-2730	RKRLQVQLSIRT	46 % (S; p < 0.01)***	NO: 1
A3	Alpha-3 chain; residues 2243-2254	KPRLQFSLDIQT	23 % (S; p < 0.01)	NO: 20
A5	Alpha-5 chain; residues 3275-3286	RNRLHLSMLVRP	22 % (S; p < 0.01)	NO: 21
C-16	Gamma-1 chain; residues 139-150	KAFDITYVRLKF	28 % (S; p < 0.01)***	NO: 2
LAM-L	Alpha-1 chain; residues 2097-2108	AASIKVAVSADR	24 % (S; p < 0.01)	NO: 22
A-13	Alpha-1 chain; residues 97-109	RQVFQVAYIIKA	30 % (S; p < 0.01)***	NO: 3
HA3G45	Alpha-3 chain; residues 1173-1184	ASFQGFQTFQPSG	21 % (S; p < 0.05)	NO: 23
HA3G47	Alpha-3 chain; residues 1189-2000	HQTWTRNLQVTL	28 % (S; p < 0.01)***	NO: 4
HA3G58	Alpha-3 chain; residues 1276-1287	ISNVFVQRLSLS	32 % (S; p < 0.01)***	NO: 5
HA3G67	Alpha-3 chain; residues 1342-1353	ASPPSVKVVQDA	25 % (S; p < 0.01)***	NO: 6
HA3G71	Alpha-3 chain; residues 1379-1390	FKLPQELLKPRS	23 % (S; p < 0.05)	NO: 24
HA3G74	Alpha-3 chain; residues 1402-1414	RGLVFHTGTKNSF	32 % (S; p < 0.01)***	NO: 7
HA3G75	Alpha-3 chain; residues 1411-1422	KNSFMALYLSKG	24 % (S; p < 0.01)	NO: 25
HA3G76	Alpha-3 chain; residues 1418-1429	YLSKGRLVFALG	26 % (S; p < 0.01)***	NO: 8
HA3G79	Alpha-3 chain; residues 1444-1455	NDGKWHTTVVFGH	27 % (S; p < 0.01)***	NO: 9
HA3G83	Alpha-3 chain; residues 1477-1487	GNSTISIRAPVY	33 % (S; p < 0.01)***	NO: 10
A4G31	Alpha-4 chain; residues 1101-1112	LHVFYDFGFSNG	23 % (S; p < 0.01)	NO: 26
A4G82	Alpha-4 chain; residues 1513-1524	TLFLAHGRLVFM	30 % (S; p < 0.01)***	NO: 11
A5G15	Alpha-5 chain; residues 2792-2803	HPDDFVFYVGGY	30 % (S; p < 0.01)***	NO: 12
A5G35	Alpha-5 chain; residues 2950-2961	VLVRVERATVFS	20 % (S; p < 0.05)	NO: 27
A5G46	Alpha-5 chain; residues 3043-3054	FLPLALPDVAPI	21 % (S; p < 0.05)	NO: 28
A5G56	Alpha-5 chain; residues 3135-3146	WLYVDDQLQLVK	27 % (S; p < 0.01)***	NO: 13
A5G71	Alpha-5 chain; residues 3259-3270	GPLPSYLQFVGI	22 % (S; p < 0.05)	NO: 29
A5G80	Alpha-5 chain; residues 3329-3340	VQSRQHSRAGQW	25 % (S; p < 0.01)***	NO: 14
A5G81	Alpha-5 chain; residues 3337-3348	AGQWHRVSVRWG	41 % (S; p < 0.01)***	NO: 15
A5G82	Alpha-5 chain; residues 3345-3356	VRWGMQQIQLVV	29 % (S; p < 0.01)***	NO: 16
A5G84	Alpha-5 chain; residues 3361-3372	TWSQKALHHRVP	27 % (S; p < 0.01)***	NO: 17
A5G101	Alpha-5 chain; residues 3516-3527	DGRWHRVAVIMG	39 % (S; p < 0.01)***	NO: 18
A5G109	Alpha-5 chain; residues 3587-3598	APVNV TASVQIQ	32 % (S; p < 0.01)***	NO: 19
A5G110	Alpha-5 chain; residues 3594-3605	SVQIQGAVGMRG	23 % (S; p < 0.05)	NO: 30

*** Selected for Further Testing

Figure 8

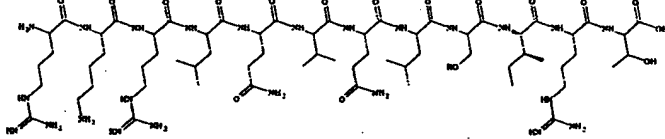
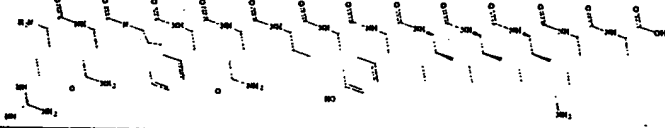
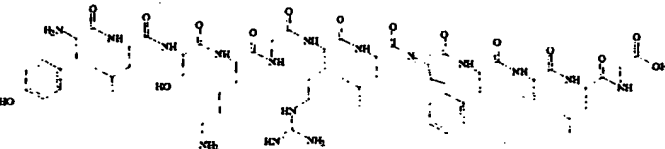
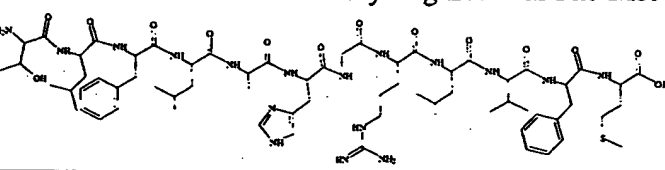
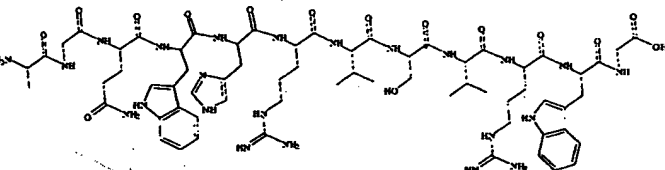
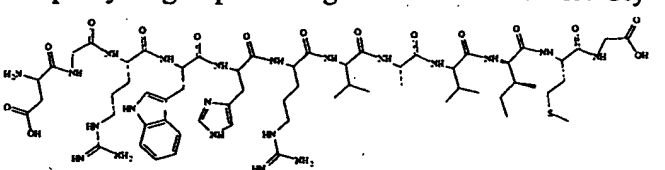
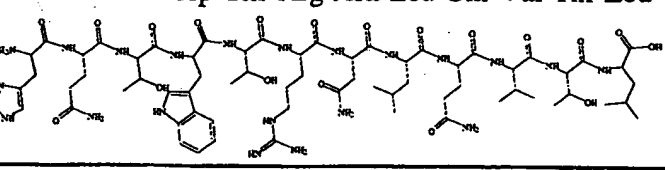
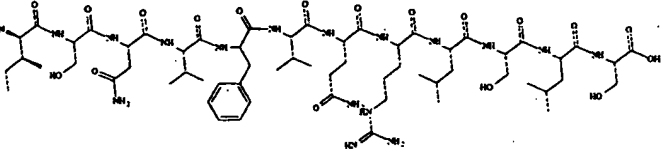
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DP-001 D-AG73 or D-A1 A1-chain 2719-2730	No: 1	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
DP-002 D-A13 A1-chain 97-109	No: 3	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala 	$C_{74}H_{121}N_{19}O_{17}$	1548.90
DP-003 D-HA3G76 A3-chain 1418-1429	No: 8	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
DP-004 D-A4G82 A4-chain 1513-1524	No: 11	Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75
DP-005 D-A5G81 A5-chain 3337-3348	No: 15	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
DP-006 D-A5G101 A5-chain 3516-3527	No: 18	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65
DP-007 D-HA3G47 A3-chain 1189-2000	No: 4	His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu 	$C_{66}H_{105}N_{21}O_{19}$	1496.70
DP-008 D-HA3G58 A3-chain 1276-1287	No: 5	Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser-Leu-Ser 	$C_{61}H_{103}N_{17}O_{18}$	1362.60

Fig. 12a

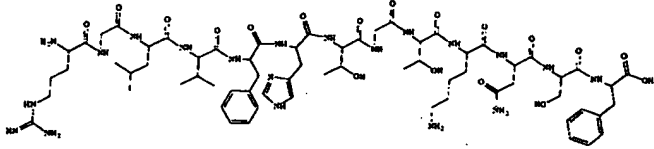
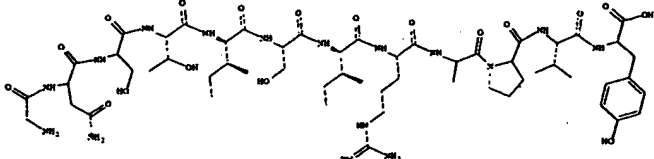
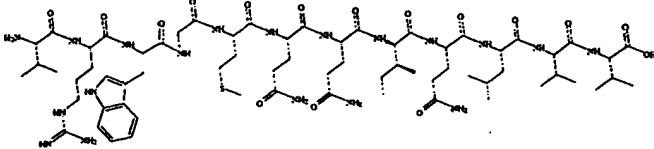
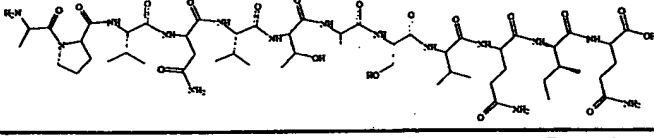
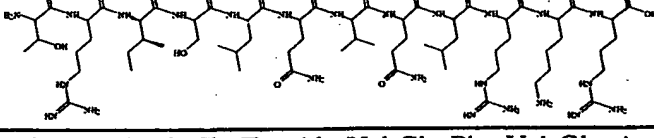
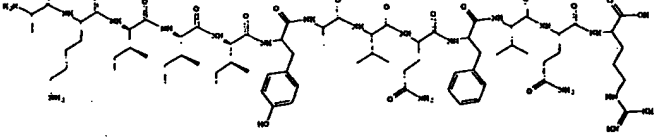
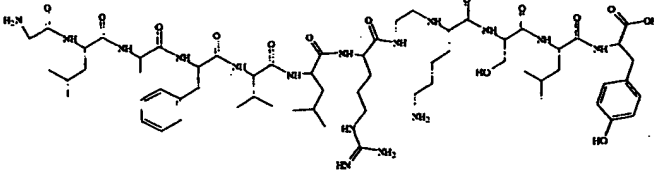
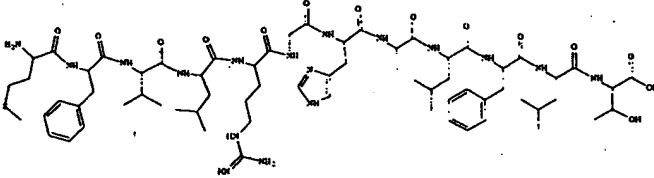
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DP-009 D-HA3G74 A3-chain 1402-1414	No: 7	Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe 	$C_{66}H_{102}N_{20}O_{18}$	1463.67
DP-010 D-HA3G83 A3-chain 1477-1487	No: 10	Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr 	$C_{56}H_{92}N_{16}O_{18}$	1277.45
DP-011 D-A5G82 A5-chain 3345-3356	No: 16	Val-Arg-Trp-Gly-Met-Gln-Gln-Ile-Gln-Leu-Val-Val 	$C_{66}H_{109}N_{19}O_{16}S$	1456.78
DP-012 D-A5G109 A3-chain 1444-1455	No: 19	Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gln-Ile-Gln 	$C_{53}H_{91}N_{15}O_{18}$	1226.40
DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or 2730-2719	No: 34	Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
DP-014 D-rA13 A1-chain r92-109 or 109-92	No: 35	Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg 	$C_{74}H_{121}N_{19}O_{17}$	1547.92
DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418	No: 36	Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513	No: 37	Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr 	$C_{67}H_{103}N_{17}O_{14}S$	1404.75

Fig. 126

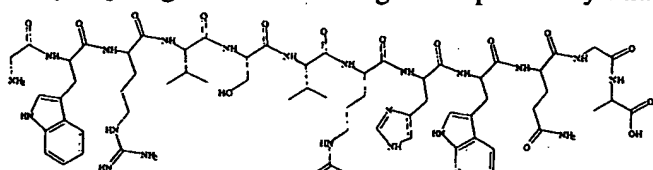
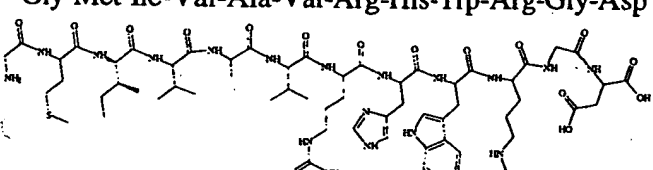
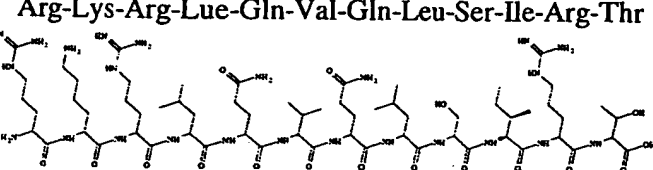
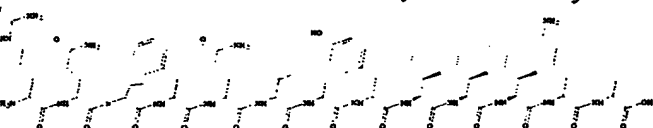
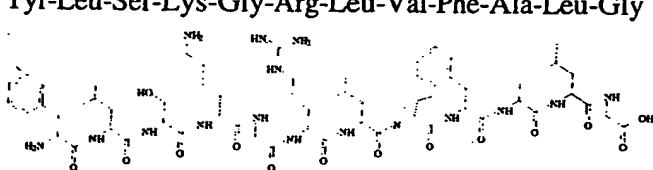
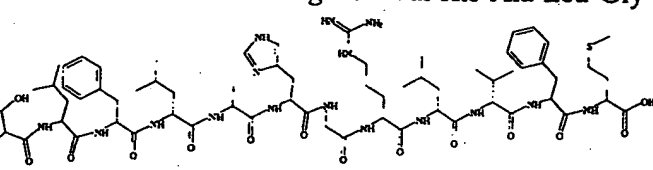
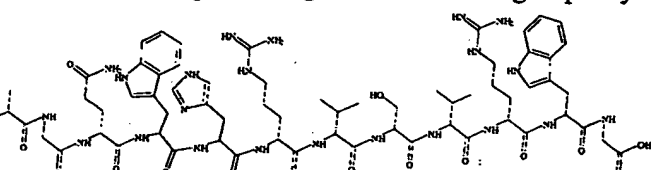
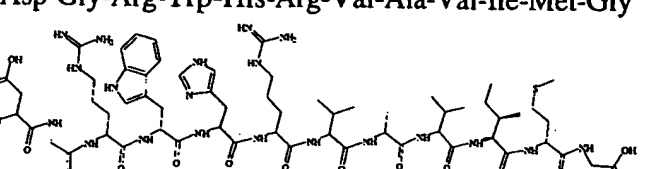
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DP-017 D-rA5G81 A5-chain r3337-3348 or 3348-3337	No: 38	Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
DP-018 D-rA5G101 A5-chain r3516-3527 or 3527-3516	No: 39	Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65
LP-019 AG73 or A1 A1-chain 2719-2730	No: 1	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
LP-020 A13 A1-chain 92-109	No: 3	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala 	$C_{74}H_{121}N_{19}O_{17}$	1548.90
LP-021 HA3G76 A3-chain 1418-1429	No: 8	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
LP-022 A4G82 A4-chain 1513-1524	No: 40	Thr-Leu-Phe-Phe-Met-Arg-Leu-Val-His-Ala-Leu-Gly 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75
LP-023 A5G81 A5-chain 3337-3348	No: 15	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
LP-024 A5G101 A5-chain 3516-3527	No: 18	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65

Fig. 12c

PTI-	SEQ ID No	Structure	Formula	MW
LP-025 β-sheet breaker or iAβ5	No: 41	Leu-Pro-Phe-Phe-Asp 	$C_{33}H_{43}N_5O_8$	637.74
DP-026 Trc'n 5;1-7	No: 42	Ala-Gly-Gln-Trp-His-Arg-Val 	$C_{38}H_{56}N_{14}O_9$	852.95
DP-027 Trc'n 5;2-8	No: 43	Gly-Gln-Trp-His-Arg-Val-Ser 	$C_{38}H_{56}N_{14}O_{10}$	868.95
DP-028 Trc'n 5;3-9	No: 44	Gln-Trp-His-Arg-Val-Ser-Val 	$C_{41}H_{62}N_{14}O_{10}$	911.04
DP-029 Trc'n 5;4-10	No: 45	Trp-His-Arg-Val-Ser-Val-Arg 	$C_{42}H_{66}N_{16}O_9$	939.09
DP-030 Trc'n 5;5-11	No: 46	His-Arg-Val-Ser-Val-Arg-Trp 	$C_{42}H_{66}N_{16}O_9$	939.09
DP-031 Trc'n 5;6-12	No: 47	Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{38}H_{62}N_{14}O_9$	859.00
DP-032 Trc'n 6;1-7	No: 48	Asp-Gly-Arg-Trp-His-Arg-Val 	$C_{40}H_{60}N_{16}O_{10}$	925.02

Fig. 12d

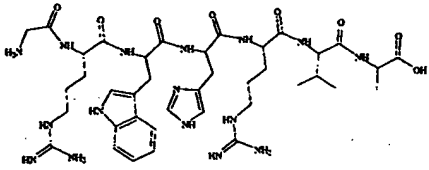
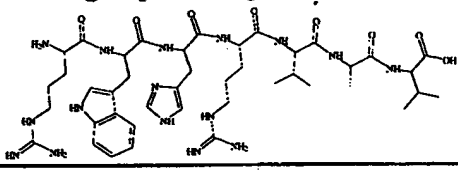
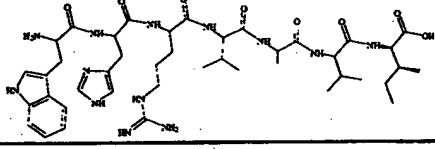
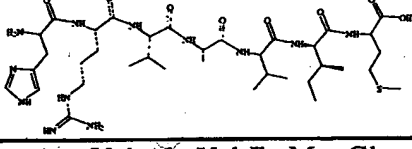
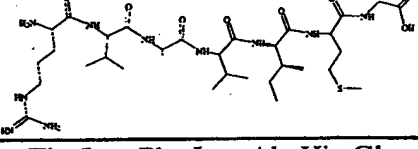
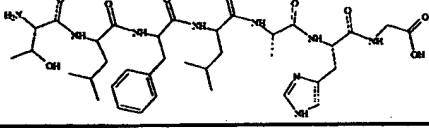
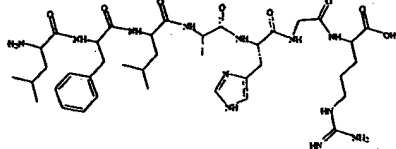
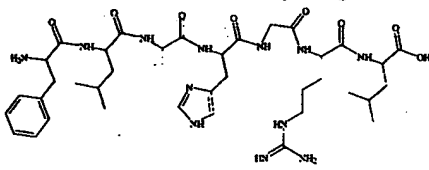
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DP-033 Trc'n 6;2-8	No: 49	<p>Gly-Arg-Trp-His-Arg-Val-Ala</p> 	$C_{39}H_{60}N_{16}O_8$	881.01
DP-034 Trc'n 6;3-9	No: 50	<p>Arg-Trp-His-Arg-Val-Ala-Val</p> 	$C_{42}H_{66}N_{16}O_8$	923.09
DP-035 Trc'n 6;4-10	No: 51	<p>Trp-His-Arg-Val-Ala-Val-Ile</p> 	$C_{42}H_{65}N_{13}O_8$	880.07
DP-036 Trc'n 6;5-11	No: 52	<p>His-Arg-Val-Ala-Val-Ile-Met</p> 	$C_{36}H_{64}N_{12}O_8S$	825.05
DP-037 Trc'n 6;6-12	No: 53	<p>Arg-Val-Ala-Val-Ile-Met-Gly</p> 	$C_{32}H_{60}N_{10}O_8S$	744.96
DP-038 Trc'n 4;1-7	No: 54	<p>Thr-Leu-Phe-Leu-Ala-His-Gly</p> 	$C_{36}H_{55}N_9O_9$	757.89
DP-039 Trc'n 4;2-8	No: 55	<p>Leu-Phe-Leu-Ala-His-Gly-Arg</p> 	$C_{38}H_{60}N_{12}O_8$	812.97
DP-040 Trc'n 4;3-9	No: 56	<p>Phe-Leu-Ala-His-Gly-Arg-Leu</p> 	$C_{38}H_{60}N_{12}O_8$	812.98

Fig. 12e

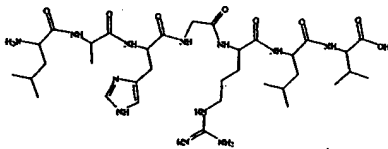
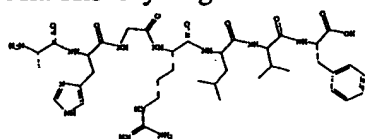
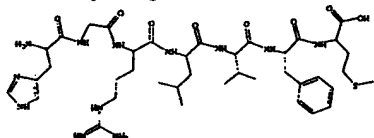
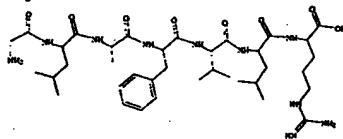
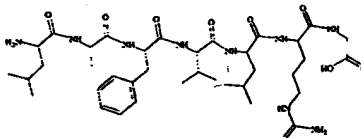
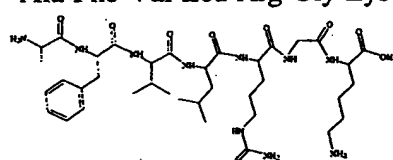
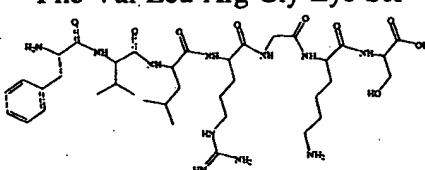
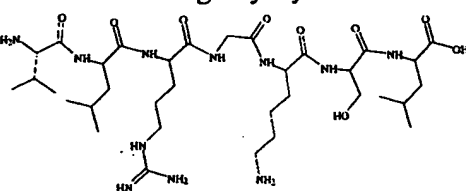
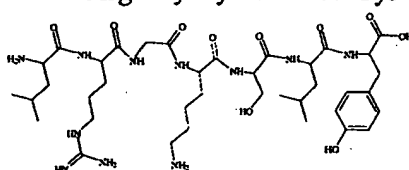
PTI-	SEQ ID NO	Structure	Formula	MW
DP-041 Trc'n 4;4-10	No: 57	Leu-Ala-His-Gly-Arg-Leu-Val 	$C_{34}H_{60}N_{12}O_8$	764.93
DP-042 Trc'n 4;5-11	No: 58	Ala-His-Gly-Arg-Leu-Val-Phe 	$C_{37}H_{58}N_{12}O_8$	798.95
DP-043 Trc'n 4;6-12	No: 59	His-Gly-Arg-Leu-Val-Phe-Met 	$C_{39}H_{62}N_{12}O_8S$	859.07
DP-044 Trc'n 15;1-7	No: 60	Gly-Leu-Ala-Phe-Val-Leu-Arg 	$C_{37}H_{62}N_{10}O_8$	774.97
DP-045 Trc'n 15;2-8	No: 61	Leu-Ala-Phe-Val-Leu-Arg-Gly 	$C_{37}H_{62}N_{10}O_8$	774.97
DP-046 Trc'n 15;3-9	No: 62	Ala-Phe-Val-Leu-Arg-Gly-Lys 	$C_{37}H_{63}N_{11}O_8$	789.98
DP-047 Trc'n 15;4-10	No: 63	Phe-Val-Leu-Arg-Gly-Lys-Ser 	$C_{37}H_{63}N_{11}O_9$	805.98
DP-048 Trc'n 15;5-11	No: 64	Val-Leu-Arg-Gly-Lys-Ser-Leu 	$C_{34}H_{65}N_{11}O_9$	771.96
DP-049 Trc'n 15;6-2	No: 65	Leu-Arg-Gly-Lys-Ser-Leu-Tyr 	$C_{38}H_{65}N_{11}O_{10}$	836.01

Fig. 12f